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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/685,258	10/14/2003	Antony Michael Carr	27866/34132B	5084

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EXAMINER	
REDDIG, PETER J	
ART UNIT	PAPER NUMBER
1642	

DATE MAILED: 11/21/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/685,258	CARR, ANTONY MICHAEL	
	Examiner	Art Unit	
	Peter J. Reddig	1642	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *September 27, 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *18 and 19* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *18 and 19* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☒ Certified copies of the priority documents have been received in Application No. 09/029,047.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *11/19/2004*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. The response filed on September 27, 2006 to the restriction requirement of July 26, 2006 has been received. Applicant has elected Group I, claims 18 and 19 drawn to a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide set out in SEQ ID NO: 1 or said polypeptide encoded by a polynucleotide encoding the amino acid sequence set out in SEQ ID NO: 2 for examination. Because applicant did not distinctly and specifically point out any supposed errors in the restriction requirement, the election has been treated as an election without traverse MPEP 818.03(a).

2. Claims 18-19 are pending.

3. Claims 18-19, drawn to a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide set out in SEQ ID NO: 3 or said polypeptide encoded by a polynucleotide encoding the amino acid sequence set out in SEQ ID NO: 4 have been withdrawn from further consideration by the examiner under 37 CFR 1.142(b) as being drawn to non-elected inventions.

5. Claims 18 and 19, drawn to a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide set out in SEQ ID NO: 1 or said polypeptide encoded a polynucleotide encoding the amino acid sequence set out in SEQ ID NO: 2 are currently under examination.

Specification

6. The disclosure is objected to because of the following informalities:

There are multiple typographical errors in the specification wherein letters appear to be missing, see p. 5, lines 2 and 3 and p. 8 line 1, for example. Please review the specification for similar typographical errors.

Appropriate correction is required.

The identifying data of all prior applications for which benefits are claimed should be provided in either the first sentence(s) of the specification or in an application data sheet. The priority data on page 1 should be updated to state that Application No. 09/029,047 is now U. S. Patent No. 6,632,936. See MPEP § 202.02.

Appropriate correction is required.

The disclosure is objected to because of the following informalities: The arrangement of the specification is incorrect, see MPEP 601. The Brief Description of the Several Views of the Drawings is out of order.

Appropriate correction is required.

The following guidelines illustrate the preferred layout for the specification of a utility application. These guidelines are suggested for the applicant's use.

Arrangement of the Specification

As provided in 37 CFR 1.77(b), the specification of a utility application should include the following sections in order. Each of the lettered items should appear in upper case, without underlining or bold type, as a section heading. If no text follows the section heading, the phrase "Not Applicable" should follow the section heading:

(a) TITLE OF THE INVENTION.
(b) CROSS-REFERENCE TO RELATED APPLICATIONS.
(c) STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT.
(d) THE NAMES OF THE PARTIES TO A JOINT RESEARCH AGREEMENT.
(e) INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ON A COMPACT DISC.

(f) BACKGROUND OF THE INVENTION.
(1) Field of the Invention.
(2) Description of Related Art including information disclosed under 37 CFR 1.97 and 1.98.
(g) BRIEF SUMMARY OF THE INVENTION.
(h) BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWING(S).
(i) DETAILED DESCRIPTION OF THE INVENTION.
(j) CLAIM OR CLAIMS (commencing on a separate sheet).
(k) ABSTRACT OF THE DISCLOSURE (commencing on a separate sheet).
(l) SEQUENCE LISTING (See MPEP § 2424 and 37 CFR 1.821-1.825. A "Sequence Listing" is required on paper if the application discloses a nucleotide or amino acid sequence as defined in 37 CFR 1.821(a) and if the required "Sequence Listing" is not submitted as an electronic document on compact disc).

Claim Rejections - 35 USC § 101

7. 35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title.

8. Claims 18 and 19 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by neither a specific, substantial asserted utility or a well-established utility. The disclosure asserts utility for the ATR polypeptide as a lipid kinase, as a target molecule for screening candidate substances for use as compounds for inhibiting or activating ATR activity (see p. 3, lines 14-18), for screening candidate substances for use as compounds for inhibiting interactions between ATR and other compounds that interact with ATR, including ATR itself, which could be used in treating cancer (see p. 3, lines 14-18 and p. 20 lines 27-28), to study the role of ATR as a checkpoint gene (p.12, lines 5-6), to be used in assay systems to identify candidate substances which interfere or enhance checkpoint functions in the cell (p.12, lines 19-21), for making antibodies to ATR (Section E, starting on p.14), and developing anti-cancer compounds that decrease the lipid kinase of ATR (p. 16, lines 21-31)

However, neither the specification nor any art of record teaches what ATR is, what it does do and do not teach a relationship to any specific diseases or establish any involvement in the etiology of any specific diseases. The asserted utilities for ATR, such as production of and screening of antibodies and antagonists apply to many unrelated polypeptide structures sequences. Therefore the asserted utilities are not considered specific utilities, i.e. they are not specific to ATR.

The asserted utility of the ATR, SEQ ID NO: 2, is based on the assertion that ATR has structural identity to Rad3. However, a review of the following database (A_Geneseq_21, Issued_Patents_AA, Published_Applications_AA_Main, Published_Applications_AA_New, PIR_80, UniProt_7.2) has revealed the identity of ATR/SEQ ID NO: 2 to RAD3 to be 14.7%. Although the specification teaches that the claimed protein has lipid kinase activity and has a role in the cell cycle checkpoint regulation, apparently because of a putative identity to RAD3, neither the specification nor the art of record what ATR is or does and does not teach any relationship to a specific disease or to an etiology of any specific disease. It is clear that given this clear lack of identity of ATR to RAD3, 14.7% identity or 85.3% lack of identity/similarity, the effects of this dissimilarity upon protein structure and function cannot be predicted.

Bowie et al (Science, 1990, 257:1306-1310, IDS) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-dimensional structures that allows them to function and carry out the instructions of the genome and further teaches that the problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex, (col 1, p. 1306). Bowie et al

further teach that while it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three dimensional structure/function relationship and these regions can tolerate only conservative substitutions or no substitutions (col 2, p. 1306). The sensitivity of proteins to alterations of even a single amino acid in a sequence are exemplified by Burgess et al (J of Cell Bio. 111:2129-2138, 1990, IDS) who teach that replacement of a single lysine reside at position 118 of acidic fibroblast growth factor by glutamic acid led to the substantial loss of heparin binding, receptor binding and biological activity of the protein and by Lazar et al (Molecular and Cellular Biology, 1988, 8:1247-1252) who teach that in transforming growth factor alpha, replacement of aspartic acid at position 47 with alanine or asparagine did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen. These references demonstrate that even a single amino acid substitution will often dramatically affect the biological activity and characteristics of a protein. Clearly, with 85.3 % dissimilarity to RAD3, the function of the ATR polypeptide could not be predicted, based on sequence similarity with RAD3, nor would it be expected to be the same as that of RAD3. Further, Scott et al (Nature Genetics, 1999, 21:440-443) teach that the gene causing Pendred syndrome encodes a putative transmembrane protein designated pendrin. Based on sequence similarity data, the authors postulated that the putative protein was deemed to be a member of sulfate transport protein family since the putative protein had a 29% identity to rat sulfate-anion transporter, 32% similarity to human diastrophic dysplasia sulfate transporter and 45% similarity to the human sulfate transporter. However, upon analyzing the expression and kinetics of the

protein, the data revealed no evidence of sulfate transport activity wherein results revealed that pendrin functioned as a transporter of chloride and iodide. Scott et al suggest that these results underscore the importance of confirming the function of newly identified gene products even when database searched reveal significant homology to proteins of known function (page 411, 1st column, 4th paragraph). In addition, Bork (Genome Research, 2000,10:398-400) clearly teaches the pitfalls associated with comparative sequence analysis for predicting protein function because of the known error margins for high-throughput computational methods. Bork specifically teaches that computational sequence analysis is far from perfect, despite the fact that sequencing itself is highly automated and accurate (p. 398, col 1). One of the reasons for the inaccuracy is that the quality of data in public sequence databases is still insufficient. This is particularly true for data on protein function. Protein function is context dependent, and both molecular and cellular aspects have to be considered (p. 398, col 2). Conclusions from the comparison analysis are often stretched with regard to protein products (p. 398, col 3). Furthermore, recent studies show that alternative splicing might affect more than 30% of human genes and the number of known post-translational modifications of gene products is increasing constantly so that complexity at protein level is enormous. Each of these modifications may change the function of respective gene products drastically (p. 399, col 1). Further, although gene annotation via sequence database searches is already a routine job, even here the error rate is considerable (p. 399, col 2). Most features predicted with an accuracy of greater than 70% are of structural nature and at best only indirectly imply a certain functionality (see legend for table 1, page 399). As more sequences are added and as errors accumulate and propagate it becomes more difficult to infer correct function from the many possibilities revealed by database search

(p. 399para bridging cols 2 and 3). The reference finally cautions that although the current methods seem to capture important features and explain general trends, 30% of those features are missing or predicted wrongly. This has to be kept in mind when processing the results further (p. 400, para bridging cols 1 and 2). The teachings of Bork are clearly illustrated by US Pub **20030105000** which specifically teaches on page 73 that the SH2 domain of Grb14 is 81% similar to the SH2 domain of Grb7 on the amino acid level, but although Grb7 binds to ErbB2, Grb14 does not bind to ErbB2. Further, although the SH2 domain of Grb2 is only 50 % similarity to Grb 7 on the amino acid level, both Grb2 and Grb7 bind to the same site on ErbB2. Thus, sequence identity or similarity alone cannot be used to predict the function of a protein.

Clearly, given not only the teachings of Bowie et al, Lazar et al and Burgess et al but also the limitations and pitfalls of using computational sequence analysis and the unknown effects of alternative splicing, post translational modification and cellular context on protein function as taught by Bork, clearly with a 85.3 % dissimilarity to RAD 3, the function of the ATR polypeptide could not be predicted, based on sequence similarity with RAD3, nor would it be expected to be the same as that of RAD3. Further, even if the ATR is related to RAD 3, neither the specification nor any art of record teaches what the polypeptide is, what it does, does not teach a relationship to any specific disease or establish any involvement of the polypeptide in the etiology of any specific disease. Given the above, it is clear that additional work must be done in order to establish that ATR functions in any manner similar to the RAD3 and thus the claimed invention does not have substantial utility. Further, given the limited identity to the members of the RAD3, it is clear, for the reasons set forth above, that ATR does not have a well-established utility based on its identity to said family.

Furthermore, while the disclosure asserts that ATR is a lipid kinase, the specification fails to assert what compounds the ATR protein phosphorylates, which is important, as kinases comprise a highly diverse group of proteins which phosphorylates a wide variety of different compounds including, proteins, carbohydrates, lipids and nucleic acids. While the specification asserts that the ATR protein is a lipid kinase, the disclosure fails to provide any disclosure of what lipids are actually phosphorylated. This is clearly insufficient to provide an expectation to a skilled artisan that they act on similar substrates. As kinases are such a large diverse family of enzymes, a mere disclosure that a protein is a kinase or a lipid kinase without a more specific recitation of what type of kinase (i.e., what lipid is phosphorylated) is insufficient to provide a substantial utility as the skilled artisan would require further research to identify or reasonably confirm a real world context of use.

Critically, although the specification asserts that ATR is a lipid kinase, additional research has revealed that ATR is in fact NOT a lipid kinase, validating the clear necessity for additional research in order to establish a functional use for the claimed ATR and the lack of substantial utility of the invention at the time the Application was filed.

In particular, Abraham (Genes & Development, 2001 15:2177-2196) teaches that despite sequence similarity to phosphoinositide kinases, ATR and related kinases transfer phosphate exclusively to protein rather than lipid substrates, see p. 2179, right column and p. 2178, left column. Furthermore, Loughney and Keegan (US Pat No. 6,344,549 1999) teach that although amino acid sequences of ATR family kinase domains are most closely related to lipid kinases, all have been shown to function as protein kinases, see column 1, lines 44-49.

Thus, it is clear that at the time the invention was made the function ATR was unknown and that additional work was required in order to establish a functional use for the claimed invention. Applicant is reminded that the utility of a claimed invention must be established at the time the invention was made in order to meet the requirements of 35 USC 101.

Further, the disclosure also lists a general use for the polypeptides encoded by the claimed polynucleotide as a target molecule in the development of pharmaceuticals. However, there is no information that links the use of the ATR polypeptide to any specific disease state. Thus the asserted utility of the claimed polypeptides and its variants is not substantial or specific because the substrate phosphorylated was unknown at the time the invention was made, the results of phosphorylation was unknown and further research to identify or reasonably confirm a real world context of use was required. The specification essentially gives an invitation to experiment wherein the artisan is invited to elaborate a functional use for the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

9. Claims 18 and 19 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

10. If applicants were able to overcome the rejections set forth above under 35 U.S.C. 112, first paragraph, claims 18 and 19 would still be rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a purified and isolated ATR polypeptide, said polypeptide encoded by a polynucleotide set out in SEQ ID NO: 1 or said polypeptide encoded by a polynucleotide encoding the amino acid sequence set out in SEQ ID NO: 2, does not reasonably provide enablement for a purified and isolated ATR polypeptide that has **lipid kinase activity**, said polypeptide encoded by a polynucleotide set out in SEQ ID NO: 1, and a polynucleotide encoding the amino acid sequence set out in SEQ ID NO: 2. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The specification teaches that the human ATR cDNA sequence is set out as Seq. ID No. 1 and the amino acid sequence of the ORF from nucleotides 80 and 8011 is set out as Seq. ID. No. 2, p. 2 lines 19-20. The specification teaches that ATR (ataxia and rad related), displays significantly higher homology to rad3 than it does to the ATM gene, p. 2, lines 16-17. The specification teaches that the C-terminal region of the rad3 protein contains a lipid kinase domain, which is required for Rad3 function, p. 2, lines 10-11. The specification teaches that the lipid kinase domain of ATR is represented by nucleotides 7054 to 8011 of Seq. ID. 1, p. 8 lines 15-16. The specification teaches that the term "lipid kinase domain" refers to a domain, which has homology to other known lipid kinases, in particular the p110 subunit of PI-3 kinase, as determined by sequence alignments, p. 8 lines 17-19.

One cannot extrapolate the teachings to the scope of the claims because the specification does not show that ATR actually functions as a lipid kinase and the art teaches that ATR does not have lipid kinase activity.

In particular, Abraham (Genes & Development, 2001 15:2177-2196) teaches that despite sequence similarity to phosphoinositide kinases, ATR and related kinases transfer phosphate exclusively to protein rather than lipid substrates, see p. 2179, right column and p. 2178, left column. Furthermore, Loughney and Keegan (US Pat No. 6,344,549 1999) teach that although amino acid sequences of ATR family kinase domains are most closely related to lipid kinases, all have been shown to function as protein kinases, see column 1, lines 44-49.

Thus, given the above, one of ordinary skill in the art would not reasonably predict that a purified and isolated ATR polypeptide, said polypeptide encoded by a polynucleotide set out in SEQ ID NO: 1 or said polypeptide encoded by a polynucleotide encoding the amino acid sequence set out in SEQ ID NO: 2 has lipid kinase activity without undue experimentation to show that it does possess this activity.

11. Claims 18 and 19 are rejected under 35 USC 112, first paragraph, as lacking an adequate written description in the specification.

Claims 18 and 19 are drawn to a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide which hybridizes to the complement of the polynucleotide of encoding the amino acid sequence set out in SEQ ID NO: 2 or a polynucleotide set out in SEQ ID NO: 1 under conditions including a final wash at 55° C. As it is drawn to the DNA arts, the findings in University of California v. Eli Lilly and Co., 119

F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." Id. At 1567, 43 USPQ2d at 1405. The court also stated that

> a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA" without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.

Id. At 1568, 43 USPQ2d at 1406. The court concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." Id.

Finally, the court addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." Id.

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that "the written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ....i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. " Id. At 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original).

Thus, the instant specification may provide an adequate written description of a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide which hybridizes to the complement of the polynucleotide of encoding the amino acid sequence set out in SEQ ID NO: 2 or a polynucleotide set out in SEQ ID NO: 1 under conditions including a final wash at 55° C, per Lilly by structurally describing a representative number of portions of said polypeptides or by describing "structural features common to the members of the genus, which features constitute a substantial portion of the genus." Alternatively, per Enzo, the specification can show that the claimed invention is complete "by disclosure of sufficiently detailed, relevant identifying characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In this case, the specification does not describe a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide which hybridizes to

the complement of the polynucleotide of encoding the amino acid sequence set out in SEQ ID NO: 2 or a polynucleotide set out in SEQ ID NO: 1 under conditions including a final wash at 55° C in a manner that satisfies either the Lilly or Enzo standards. The specification does not provide the complete structure of a portion of said polypeptides nor any functional characteristics coupled with a known or disclosed correlation between structure and function. Although the specification discloses SEQ ID NO: 2, this does not provide a description of a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide which hybridizes to the complement of the polynucleotide of encoding the amino acid sequence set out in SEQ ID NO: 2 or a polynucleotide set out in SEQ ID NO: 1 under conditions including a final wash at 55° C that would satisfy the standard set out in Enzo.

The specification also fails to describe a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide which hybridizes to the complement of the polynucleotide of encoding the amino acid sequence set out in SEQ ID NO: 2 or a polynucleotide set out in SEQ ID NO: 1 under conditions including a final wash at 55° C by the test set out in Lilly. The specification describes only a SEQ ID NO: 2. Therefore, it necessarily fails to describe a "representative number" of such species. In addition, the specification also does not describe "structural features common to the members of the genus, which features constitute a substantial portion of the genus."

Thus, the specification does not provide an adequate written description of a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by a polynucleotide which hybridizes to the complement of the polynucleotide of encoding the amino

acid sequence set out in SEQ ID NO: 2 or a polynucleotide set out in SEQ ID NO: 1 under conditions including a final wash at 55° C that is required to practice the claimed invention.

12. Claim 19 is rejected under 35 USC 112, first paragraph, as lacking an adequate written description in the specification.

Claim 19 is drawn to a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by **a** polynucleotide set out in SEQ ID NO: 1, which reads on a polypeptide that is encoded by only a portion of said polynucleotide and which reads on polypeptides that comprise as little as two encoded amino acids. As it is drawn to the DNA arts, the findings in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." Id. At 1567, 43 USPQ2d at 1405. The court also stated that

> a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA" without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.

Id. At 1568, 43 USPQ2d at 1406. The court concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." Id.

Finally, the court addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." Id.

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that "the written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ....i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. " Id. At 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original).

Thus, the instant specification may provide an adequate written description of a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by **a** polynucleotide set out in SEQ ID NO: 1, per Lilly by structurally describing a representative number of portions of said polypeptides or by describing "structural features common to the members of the genus, which features constitute a substantial portion of the genus."

Alternatively, per Enzo, the specification can show that the claimed invention is complete "by disclosure of sufficiently detailed, relevant identifying characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In this case, the specification does not describe a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by **a** polynucleotide set out in SEQ ID NO: 1in a manner that satisfies either the Lilly or Enzo standards. The specification does not provide the complete structure of a portion of said polypeptides nor any functional characteristics coupled with a known or disclosed correlation between structure and function. Although the specification discloses SEQ ID NO: 2, this does not provide a description of a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by **a** polynucleotide set out in SEQ ID NO: 1 that would satisfy the standard set out in Enzo.

The specification also fails to describe a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by **a** polynucleotide set out in SEQ ID NO: 1 by the test set out in Lilly. The specification describes only a SEQ ID NO: 2. Therefore, it necessarily fails to describe a "representative number" of such species. In addition, the specification also does not describe "structural features common to the members of the genus, which features constitute a substantial portion of the genus."

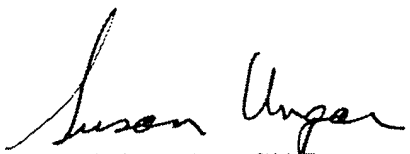
Thus, the specification does not provide an adequate written description of a purified and isolated ATR polypeptide that has lipid kinase activity, said polypeptide encoded by **a** **polynucleotide** set out in SEQ ID NO: 1 that is required to practice the claimed invention.

13. No claims are allowed.

14. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Peter J. Reddig whose telephone number is (571) 272-9031. The examiner can normally be reached on M-F 8:30 a.m.-5:00 p.m..

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jeffrey Siew can be reached on (571) 272-0787. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.



SUSAN UNGAR, PH.D
PRIMARY EXAMINER

Peter J. Reddig, Ph.D.
Examiner
Art Unit 1642

PJR